SEQUENCE LISTING

```
<110> DIXON, RICHARD A.
      LIU, CHANG-JUN
     DEAVOURS, BETTINA
<120> METHODS AND COMPOSITIONS FOR PRODUCTION OF FLAVONOID
      AND ISOFLAVONOID NUTRACEUTICALS
<130> NBLE:007US
<140> UNKNOWN
<141> 2003-09-10
<150> 60/409,447
<151> 2002-09-10
<160> 14
<170> PatentIn Ver. 2.1
<210> 1
<211> 1824
<212> DNA
<213> Soybean
<400> 1
ggaaaattag cctcacaaaa gcaaagatca aacaaaccaa ggacgagaac acgatgttgc 60
ttgaacttgc acttggttta ttggttttgg ctctgtttct gcacttgcgt cccacaccca 120
ctqcaaaatc aaaaqcactt cqccatctcc caaacccacc aagcccaaag cctcgtcttc 180
ccttcatagg acaccttcat ctcttaaaag acaaacttct ccactacgca ctcatcgacc 240
tctccaaaaa acatggtccc ttattctctc tctactttgg ctccatgcca accgttgttg 300
cctccacacc agaattqttc aagctcttcc tccaaacgca cgaggcaact tccttcaaca 360
caaggttcca aacctcagcc ataagacgcc tcacctatga tagctcagtg gccatggttc 420
ccttcggacc ttactggaag ttcgtgagga agctcatcat gaacgacctt cccaacgcca 480
ccactgtaaa caagttgagg cctttgagga cccaacagac ccgcaagttc cttagggtta 540
ccaacagcac catctccatg atgatgctcg gcgaggctga ggagatcaga gacatcgctc 660
gegaggttet taagatettt ggegaataca geeteactga etteatetgg eeattgaage 720
atctcaaggt tggaaagtat gagaagagga tcgacgacat cttgaacaag ttcgaccctg 780
tcgttgaaag ggtcatcaag aagcgccgtg agatcgtgag gaggagaaag aacggagagg 840
ttqttqaqqq tqaqqtcaqc ggggttttcc ttgacacttt gcttgaattc gctgaggatg 900
agaccatgga gatcaaaatc accaaggacc acatcgaggg tcttgttgtc gactttttct 960
cggcaggaac agactccaca gcggtggcaa cagagtgggc attggcagaa ctcatcaaca 1020
atcctaaggt gttggaaaag gctcgtgagg aggtctacag tgttgtggga aaggacagac 1080
ttgtggacga agttgacact caaaaccttc cttacattag agcaatcgtg aaggagacat 1140
tccgcatgca cccgccactc ccagtggtca aaagaaagtg cacagaagag tgtgagatta 1200
atggatatgt gatcccagag ggagcattga ttctcttcaa tgtatggcaa gtaggaagag 1260
accccaaata ctgggacaga ccatcggagt tccgtcctga gaggttccta gagacagggg 1320
ctgaagggga agcagggcct cttgatctta ggggacaaca ttttcaactt ctcccatttg 1380
ggtctgggag gagaatgtgc cctggagtca atctggctac ttcgggaatg gcaacacttc 1440
ttgcatctct tattcagtgc ttcgacttgc aagtgctggg tccacaagga cagatattga 1500
agggtggtga cgccaaagtt agcatggaag agagagccgg cctcactgtt ccaagggcac 1560
atagtettgt etgtgtteca ettgeaagga teggegttge atetaaaete etttettaat 1620
```

taagatcatc atcatatata atatttactt tttgtgtgtt gataatcatc atttcaataa 1680 ggtctcgttc atctactttt tatgaagtat ataagccctt ccatgcacat tgtatcatct 1740 cccatttgtc ttcgtttgct acctaaggca atctttttt ttttagaatc acatcatcct 1800

<210> 2 <211> 521 <212> PRT

<213> Soybean

<400> 2

Met Leu Leu Glu Leu Ala Leu Gly Leu Leu Val Leu Ala Leu Phe Leu 1 5 10 15

His Leu Arg Pro Thr Pro Thr Ala Lys Ser Lys Ala Leu Arg His Leu
20 25 30

Pro Asn Pro Pro Ser Pro Lys Pro Arg Leu Pro Phe Ile Gly His Leu
35 40 45

His Leu Leu Lys Asp Lys Leu Leu His Tyr Ala Leu Ile Asp Leu Ser
50 60

Lys Lys His Gly Pro Leu Phe Ser Leu Tyr Phe Gly Ser Met Pro Thr 65 70 75 80

Val Val Ala Ser Thr Pro Glu Leu Phe Lys Leu Phe Leu Gln Thr His
85 90 95

Glu Ala Thr Ser Phe Asn Thr Arg Phe Gln Thr Ser Ala Ile Arg Arg
100 105 110

Leu Thr Tyr Asp Ser Ser Val Ala Met Val Pro Phe Gly Pro Tyr Trp 115 120 125

Lys Phe Val Arg Lys Leu Ile Met Asn Asp Leu Pro Asn Ala Thr Thr 130 135 140

Val Asn Lys Leu Arg Pro Leu Arg Thr Gln Gln Thr Arg Lys Phe Leu 145 150 155 160

Arg Val Met Ala Gln Gly Ala Glu Ala Gln Lys Pro Leu Asp Leu Thr
165 170 175

Glu Glu Leu Leu Lys Trp Thr Asn Ser Thr Ile Ser Met Met Leu 180 185 190

Gly Glu Ala Glu Glu Ile Arg Asp Ile Ala Arg Glu Val Leu Lys Ile 195 200 205

Phe Gly Glu Tyr Ser Leu Thr Asp Phe Ile Trp Pro Leu Lys His Leu 210 215 220

Lys Val Gly Lys Tyr Glu Lys Arg Ile Asp Asp Ile Leu Asn Lys Phe 225 230 235 240

Asp Pro Val Val Glu Arg Val Ile Lys Lys Arg Arg Glu Ile Val Arg 245 250 255

Arg Arg Lys Asn Gly Glu Val Val Glu Glu Val Ser Gly Val Phe
260 265 270

Leu Asp Thr Leu Leu Glu Phe Ala Glu Asp Glu Thr Met Glu Ile Lys
275
280
285

Ile Thr Lys Asp His Ile Glu Gly Leu Val Val Asp Phe Phe Ser Ala 290 295 300

Gly Thr Asp Ser Thr Ala Val Ala Thr Glu Trp Ala Leu Ala Glu Leu 305 310 315 320

Ile Asn Asn Pro Lys Val Leu Glu Lys Ala Arg Glu Glu Val Tyr Ser 325 330 335

Val Val Gly Lys Asp Arg Leu Val Asp Glu Val Asp Thr Gln Asn Leu 340 345 350

Pro Tyr Ile Arg Ala Ile Val Lys Glu Thr Phe Arg Met His Pro Pro 355 360 365

Leu Pro Val Val Lys Arg Lys Cys Thr Glu Glu Cys Glu Ile Asn Gly 370 375 380

Tyr Val Ile Pro Glu Gly Ala Leu Ile Leu Phe Asn Val Trp Gln Val 385 390 395 400

Gly Arg Asp Pro Lys Tyr Trp Asp Arg Pro Ser Glu Phe Arg Pro Glu 405 410 415

Arg Phe Leu Glu Thr Gly Ala Glu Gly Glu Ala Gly Pro Leu Asp Leu 420 425 430

Arg Gly Gln His Phe Gln Leu Leu Pro Phe Gly Ser Gly Arg Arg Met 435 440 445

Cys Pro Gly Val Asn Leu Ala Thr Ser Gly Met Ala Thr Leu Leu Ala 450 455 460

Ser Leu Ile Gln Cys Phe Asp Leu Gln Val Leu Gly Pro Gln Gly Gln 465 470 475 480

Ile Leu Lys Gly Gly Asp Ala Lys Val Ser Met Glu Glu Arg Ala Gly
485 490 495

Leu Thr Val Pro Arg Ala His Ser Leu Val Cys Val Pro Leu Ala Arg 500 505 510

Ile Gly Val Ala Ser Lys Leu Leu Ser 515 520

<210> 3

<211> 950

<212> DNA

<213> Medicago sativa

<220> <221> CDS <222> (41)..(709)

40															
	0> 3 ttcc	cat a	agcta	aaac	aa aa	aaaa	attaa	a gaa	acaa	gaat		gct Ala			55
												gtg Val			103
												ggg Gly			151
_			_								_	ata Ile 50	 		199
												tgg Trp			247
		_										aga Arg			295
												att Ile			343
												tgt Cys		-	391
												gaa Glu 130			439
		_	_	_		_		-				cct Pro	 _		487
												ctt Leu			535
												ata Ile			583
												gag Glu			631

tcc cct gat ctt aag cgc tgt tta gct gca aga tta cct gcg ttg ttg 679 Ser Pro Asp Leu Lys Arg Cys Leu Ala Ala Arg Leu Pro Ala Leu Leu 200 205 210

aac gag ggt gct ttc aag att gga aac tga tgatgattat actcctatat 729 Asn Glu Gly Ala Phe Lys Ile Gly Asn 215 220

<210> 4 <211> 222 <212> PRT <213> Medicago sativa

<400> 4 Met Ala Ala Ser Ile Thr Ala Ile Thr Val Glu Asn Leu Glu Tyr Pro Ala Val Val Thr Ser Pro Val Thr Gly Lys Ser Tyr Phe Leu Gly Gly 25 Ala Gly Glu Arg Gly Leu Thr Ile Glu Gly Asn Phe Ile Lys Phe Thr 40 Ala Ile Gly Val Tyr Leu Glu Asp Ile Ala Val Ala Ser Leu Ala Ala 55 60 Lys Trp Lys Gly Lys Ser Ser Glu Glu Leu Leu Glu Thr Leu Asp Phe 70 75 Tyr Arg Asp Ile Ile Ser Gly Pro Phe Glu Lys Leu Ile Arg Gly Ser 85 90 Lys Ile Arg Glu Leu Ser Gly Pro Glu Tyr Ser Arg Lys Val Met Glu 100 105 110 Asn Cys Val Ala His Leu Lys Ser Val Gly Thr Tyr Gly Asp Ala Glu 125 120 Ala Glu Ala Met Gln Lys Phe Ala Glu Ala Phe Lys Pro Val Asn Phe 135 Pro Pro Gly Ala Ser Val Phe Tyr Arg Gln Ser Pro Asp Gly Ile Leu 150 155 Gly Leu Ser Phe Ser Pro Asp Thr Ser Ile Pro Glu Lys Glu Ala Ala 165 170 Leu Ile Glu Asn Lys Ala Val Ser Ser Ala Val Leu Glu Thr Met Ile 185 Gly Glu His Ala Val Ser Pro Asp Leu Lys Arg Cys Leu Ala Ala Arg 200 Leu Pro Ala Leu Leu Asn Glu Gly Ala Phe Lys Ile Gly Asn

220

<210> 5 <211> 836 <212> DNA

210

25334885.1

215

<213> Medicago sativa

```
caaatcatat ttcctcggtg gcgctgggga gagaggattg accattgaag gaaacttcat 60
caagttcact gccataggtg tttatttgga agatatagca gtggcttcac tagctgccaa 120
atggaagggt aaatcatctg aagagttact tgagaccctt gacttttaca gagacatcat 180
ctcaggtccc tttgaaaagt taattagagg gtcaaagatt agggaattga gtggtcctga 240
gtactcaagg aaggttatgg agaactgtgt ggcacacttg aaatcagttg gaacttatgg 300
agatgcagaa gctgaagcta tgcaaaaatt tgctgaagct ttcaagcctg ttaattttcc 360
acctggtgcc tctgttttct acaggcaatc acctgatgga atattagggc ttagtttctc 420
tccggataca agtataccag aaaaggaggc tgcactcata gagaacaagg cagtttcatc 480
agcagtgttg gagactatga teggegaaca egetgtttee eetgatetta agegetgttt 540
ggctgcaaga ttacctgcgt tgttgaacqa gggtgctttc aagattggaa actgatgatg 600
attatactct tatataaaaa catttccaaa agcgttgcag cacaagaatg agaccatgga 660
cttttttaag totacacgtt taattttttg tatatotatt taccttctta ttagtatoaa 720
tagtatgaaa tgaaagatct tgctttctac tcttgtacta tttctgtgat agataatgtt 780
aatgagtatc ttcatcaata aaagtgattt gttttgtttg ttcaaaaaaa aaaaaa
<210> 6
<211> 1380
<212> DNA
<213> Medicago sativa
<220>
<221> CDS
<222> (67)..(1236)
<400> 6
gaattcccaa caaacaagta ctgcaaacca attgagtatt acatagaaac tactagagat 60
accaag atg gtg agt gta tct gaa att cgc aag gct cag agg gca gaa
                                                                   108
       Met Val Ser Val Ser Glu Ile Arg Lys Ala Gln Arg Ala Glu
         1
ggt cet gca acc att ttg gcc att ggc act gca aat cca gca aat tgt
                                                                   156
Gly Pro Ala Thr Ile Leu Ala Ile Gly Thr Ala Asn Pro Ala Asn Cys
15
                     20
                                                             30
gtt gaa caa agt aca tat cct gat ttt tac ttt aaa atc aca aat agc
                                                                   204
Val Glu Gln Ser Thr Tyr Pro Asp Phe Tyr Phe Lys Ile Thr Asn Ser
gag cac aag act gaa ctc aaa gag aaa ttc caa cgc atg tgt gat aaa
                                                                   252
Glu His Lys Thr Glu Leu Lys Glu Lys Phe Gln Arg Met Cys Asp Lys
tct atg atc aag agg aga tac atg tac cta aca gag gag att ttg aaa
                                                                   300
Ser Met Ile Lys Arg Arg Tyr Met Tyr Leu Thr Glu Glu Ile Leu Lys
                             70
gag aat cct agt gtt tgt gaa tat atg gca cct tca ttg gat gcc agg
Glu Asn Pro Ser Val Cys Glu Tyr Met Ala Pro Ser Leu Asp Ala Arg
                         85
                                                                   396
caa gac atg gtg gtg gta gag gta cct aga cta ggg aag gag gct gca
Gln Asp Met Val Val Val Glu Val Pro Arg Leu Gly Lys Glu Ala Ala
```

95					100					105					110	
					gaa Glu											444
					aca Thr											492
					ttg Leu			_							_	540
					tgc Cys											588
	_	_	_		aac Asn 180					_	_	_	-	_	-	636
	_	_		_	gtc Val			_			_	_			-	684
					caa Gln											732
	_			_	cca Pro	_		_								780
_	_			-	caa Gln			_		_	_	-				828
					gaa Glu 260											876
_				_	tca Ser	_			_		_		_	-	-	924
					att Ile											972
					gca Ala											1020
_	_		_	_	atg Met	_	_		_	_			_	_		1068

```
gga aat atg tca agt gca tgt gtt ttg ttt atc tta gat gaa atg aga
                                                                1116
Gly Asn Met Ser Ser Ala Cys Val Leu Phe Ile Leu Asp Glu Met Arg
335
aag aaa tca act caa gat gga ctg aag aca aca gga gaa gga ctt gaa
                                                                 1164
Lys Lys Ser Thr Gln Asp Gly Leu Lys Thr Thr Gly Glu Gly Leu Glu
               355
                                   360
tgq gqt gtg tta ttt ggc ttt gga cca gga ctt acc ata gaa act gtt
                                                                 1212
Trp Gly Val Leu Phe Gly Phe Gly Pro Gly Leu Thr Ile Glu Thr Val
                               375
Val Leu Arg Ser Val Ala Ile
ctttcaaatt tgcttgattt ttatgtaagg atgaaaaact cgtctacagt tcaacattta 1326
ctgtcatatt aaaaataata caattgtgat tccctttaaa aaaaaaagga attc
                                                                1380
<210> 7
<211> 389
<212> PRT
<213> Medicago sativa
<400> 7
Met Val Ser Val Ser Glu Ile Arg Lys Ala Gln Arg Ala Glu Gly Pro
                                    10
Ala Thr Ile Leu Ala Ile Gly Thr Ala Asn Pro Ala Asn Cys Val Glu
                                25
Gln Ser Thr Tyr Pro Asp Phe Tyr Phe Lys Ile Thr Asn Ser Glu His
                                                45
                            40
Lys Thr Glu Leu Lys Glu Lys Phe Gln Arg Met Cys Asp Lys Ser Met
                        55
                                            60
Ile Lys Arg Arg Tyr Met Tyr Leu Thr Glu Glu Ile Leu Lys Glu Asn
                    70
                                        75
Pro Ser Val Cys Glu Tyr Met Ala Pro Ser Leu Asp Ala Arg Gln Asp
Met Val Val Glu Val Pro Arg Leu Gly Lys Glu Ala Ala Val Lys
                               105
Ala Ile Lys Glu Trp Gly Gln Pro Lys Ser Lys Ile Thr His Leu Ile
                           120
       115
Val Cys Thr Thr Ser Gly Val Asp Met Pro Gly Ala Asp Tyr Gln Leu
                       135
Thr Lys Leu Leu Gly Leu Arg Pro Tyr Val Lys Arg Tyr Met Met Tyr
                   150
                                       155
Gln Gln Gly Cys Phe Ala Gly Gly Thr Val Leu Arg Leu Ala Lys Asp
                                   170
               165
Leu Ala Glu Asn Asn Lys Gly Ala Arg Val Leu Val Val Cys Ser Glu
                               185
                                                  190
Val Thr Ala Val Thr Phe Arg Gly Pro Ser Asp Thr His Leu Asp Ser
                           200
                                              205
Leu Val Gly Gln Ala Leu Phe Gly Asp Gly Ala Ala Ala Leu Ile Val
                       215
                                           220
Gly Ser Asp Pro Val Pro Glu Ile Glu Lys Pro Ile Phe Glu Met Val
```

```
225
                     230
                                         235
                                                              240
Trp Thr Ala Gln Thr Ile Ala Pro Asp Ser Glu Gly Ala Ile Asp Gly
                245
                                     250
His Leu Arg Glu Ala Gly Leu Thr Phe His Leu Leu Lys Asp Val Pro
                                 265
Gly Ile Val Ser Lys Asn Ile Asp Lys Ala Leu Val Glu Ala Phe Gln
                                                 285
                             280
Pro Leu Gly Ile Ser Asp Tyr Asn Ser Ile Phe Trp Ile Ala His Pro
                         295
                                             300
Gly Gly Pro Ala Ile Leu Asp Gln Val Glu Gln Lys Leu Ala Leu Lys
                    310
                                         315
Pro Glu Lys Met Arg Ala Thr Arg Glu Val Leu Ser Glu Tyr Gly Asn
                325
                                     330
Met Ser Ser Ala Cys Val Leu Phe Ile Leu Asp Glu Met Arg Lys Lys
Ser Thr Gln Asp Gly Leu Lys Thr Thr Gly Glu Gly Leu Glu Trp Gly
Val Leu Phe Gly Phe Gly Pro Gly Leu Thr Ile Glu Thr Val Val Leu
                        375
                                             380
Arg Ser Val Ala Ile
385
<210> 8
<211> 1423
<212> DNA
<213> Medicago sativa
<220>
<221> CDS
<222> (106)..(1275)
<400> 8
cgaattccca actaagtact gtaaaccata gagttcaaat tacagtactt tactttcatt 60
tgataccaac ctaccatatc attgctacac agaaactata tcaag atg gtg agt gta 117
                                                   Met Val Ser Val
tot gaa att ogt cag got caa agg goa gaa ggo oot goa acc atc atg
                                                                   165
Ser Glu Ile Arg Gln Ala Gln Arg Ala Glu Gly Pro Ala Thr Ile Met
gcc att ggc act gca aat cca tcc aac tgt gtt gaa caa agc aca tat
                                                                   213
Ala Ile Gly Thr Ala Asn Pro Ser Asn Cys Val Glu Gln Ser Thr Tyr
                 25
cct gat ttc tac ttc aaa atc aca aac agt gag cac aaa gtt gaa ctc
                                                                   261
Pro Asp Phe Tyr Phe Lys Ile Thr Asn Ser Glu His Lys Val Glu Leu
             40
                                                      50
aaa gag aaa ttt caa cgc atg tgt gat aaa tcc atg atc aag agg aga
                                                                   309
Lys Glu Lys Phe Gln Arg Met Cys Asp Lys Ser Met Ile Lys Arg Arg
         55
tac atg tat ctt acc gaa gag att ttg aaa gaa aat cca agt gta tgt
```

Tyr	Met 70	Tyr	Leu	Thr	Glu	Glu 75	Ile	Leu	Lys	Glu	Asn 80	Pro	Ser	Val	Cys	
					tca Ser 90											405
					gga Gly											453
					tca Ser											501
					cct Pro											549
					gtg Val											597
					gtc Val 170											645
					gtg Val											693
					agt Ser											741
					ggt Gly											789
		_			aaa Lys					_	_			_		837
					agt Ser 250											885
					cac His											933
					gca Ala											981
					atc Ile											1029

295 300 305

					gaa Glu											1077
					gta Val 330											1125
					tta Leu											1173
					gga Gly											1221
					acc Thr											1269
ata Ile	tga 390	aatg	gatto	gat t	gttt	tatt	t ta	ttgt	atta	ctt	ttaa	act	tgct	tgaa	at	1325
tccatgtaag aataaataca gagttcatgt accatggatg ttaaaacgaa tataccattt 13															1385	
gtag															1423	
<210> 9 <211> 389 <212> PRT <213> Medicago sativa																
<211 <212	l> 38 ?> PF	ΥT	igo s	sativ	<i>r</i> a											
<211 <212 <213 <400	L> 38 2> PF B> Me	RT edica			⁄a Glu	Ile	Arg	Gln	Ala	Gln	Arg	Ala	Glu	Gly	Pro	
<211 <212 <213 <400 Met	L> 38 2> PF 3> Me 0> 9 Val	RT edica Ser	Val Met	Ser 5			7	Ala	10				Cys	15		
<211 <212 <213 <400 Met 1 Ala	l> 38 2> PF 3> Me 0> 9 Val	RT edica Ser Ile Thr	Val Met 20 Tyr	Ser 5 Ala Pro	Glu Ile Asp	Gly Phe	Thr Tyr	Ala 25 Phe	10 Asn Lys	Pro Ile	Ser Thr	Asn Asn	Cys 30	15 Val	Glu	
<211 <212 <213 <400 Met 1 Ala	1> 38 2> PF 3> Me 3> Me Thr Ser Val	RT edica Ser Ile Thr 35	Val Met 20 Tyr	Ser 5 Ala Pro	Glu Ile	Gly Phe Lys	Thr Tyr 40	Ala 25 Phe	10 Asn Lys	Pro Ile	Ser Thr	Asn Asn 45	Cys 30 Ser	15 Val Glu	Glu His	
<211 <212 <213 <400 Met 1 Ala Gln Lys	<pre>L> 38 2> PF 3> Me Val Thr Ser Val 50</pre>	Ser Ile Thr 35	Val Met 20 Tyr Leu	Ser 5 Ala Pro Lys	Glu Ile Asp Glu Met	Gly Phe Lys 55	Thr Tyr 40 Phe	Ala 25 Phe Gln	10 Asn Lys Arg	Pro Ile Met Glu	Ser Thr Cys 60	Asn Asn 45 Asp	Cys 30 Ser Lys	15 Val Glu Ser	Glu His Met Asn	
<211 <212 <213 <400 Met 1 Ala Gln Lys Ile 65	l> 38 2> PF 3> Me 3> 9 Val Thr Ser Val 50 Lys	Ser Ile Thr 35 Glu Arg	Val Met 20 Tyr Leu Arg	Ser 5 Ala Pro Lys Tyr	Glu Ile Asp Glu	Gly Phe Lys 55 Tyr	Thr Tyr 40 Phe	Ala 25 Phe Gln Thr	10 Asn Lys Arg Glu Ser	Pro Ile Met Glu 75	Ser Thr Cys 60 Ile	Asn Asn 45 Asp Leu	Cys 30 Ser Lys	15 Val Glu Ser Glu Gln	Glu His Met Asn 80	
<211 <212 <213 <400 Met 1 AAla Gln Lys Ile 65 Pro	l> 38 2> PF 3> Me 3> Me Val Thr Ser Val 50 Lys Ser	Ser Ile Thr 35 Glu Arg	Val Met 20 Tyr Leu Arg Cys Val	Ser 5 Ala Pro Lys Tyr Glu 85	Glu Ile Asp Glu Met 70	Gly Phe Lys 55 Tyr Met	Thr Tyr 40 Phe Leu Ala	Ala 25 Phe Gln Thr	10 Asn Lys Arg Glu Ser 90	Pro Ile Met Glu 75 Leu	Ser Thr Cys 60 Ile Asp	Asn Asn 45 Asp Leu Ala	Cys 30 Ser Lys Lys Arg	15 Val Glu Ser Glu Gln 95	Glu His Met Asn 80 Asp	
<211 <212 <213 <400 Met 1 Ala Gln Lys Ile 65 Pro Met	l> 38 2> PF 3> Me 0> 9 Val Thr Ser Val 50 Lys Ser Val	Ser Ile Thr 35 Glu Arg Val	Val Met 20 Tyr Leu Arg Cys Val 100	Ser 5 Ala Pro Lys Tyr Glu 85 Glu	Glu Ile Asp Glu Met 70 Tyr	Gly Phe Lys 55 Tyr Met Pro	Thr Tyr 40 Phe Leu Ala Arg	Ala 25 Phe Gln Thr Pro Leu 105	10 Asn Lys Arg Glu Ser 90 Gly	Pro Ile Met Glu 75 Leu Lys	Ser Thr Cys 60 Ile Asp Glu	Asn 45 Asp Leu Ala	Cys 30 Ser Lys Lys Arg Ala 110	15 Val Glu Ser Glu Gln 95 Val	Glu His Met Asn 80 Asp	
<211 <212 <213 <400 Met 1 Ala Gln Lys Ile 65 Pro Met Ala	l> 38 2> PF 3> Me 0> 9 Val Thr Ser Val Lys Ser Val Ile	Ser Ile Thr 35 Glu Arg Val Val Lys 115	Val Met 20 Tyr Leu Arg Cys Val 100 Glu	Ser 5 Ala Pro Lys Tyr Glu 85 Glu	Glu Ile Asp Glu Met 70 Tyr	Gly Phe Lys 55 Tyr Met Pro Gln	Thr Tyr 40 Phe Leu Ala Arg Pro 120	Ala 25 Phe Gln Thr Pro Leu 105 Lys	10 Asn Lys Arg Glu Ser 90 Gly Ser	Pro Ile Met Glu 75 Leu Lys	Ser Thr Cys 60 Ile Asp Glu Ile	Asn Asn 45 Asp Leu Ala Ala Thr 125	Cys 30 Ser Lys Lys Arg Ala 110 His	15 Val Glu Ser Glu Gln 95 Val Leu	Glu His Met Asn 80 Asp Lys Ile	

```
Gln Gln Gly Cys Phe Ala Gly Gly Thr Val Leu Arg Leu Ala Lys Asp
                 165
                                     170
Leu Ala Glu Asn Asn Lys Gly Ala Arg Val Leu Val Val Cys Ser Glu
                                 185
                                                      190
Val Thr Ala Val Thr Phe Arg Gly Pro Ser Asp Thr His Leu Asp Ser
                             200
Leu Val Gly Gln Ala Leu Phe Gly Asp Gly Ala Ala Ala Leu Ile Val
                         215
                                             220
Gly Ser Asp Pro Ile Pro Glu Ile Glu Lys Pro Ile Phe Glu Met Val
                    230
                                         235
Trp Thr Ala Gln Thr Ile Ala Pro Asp Ser Glu Gly Ala Ile Asp Gly
                245
                                     250
His Leu Val Glu Ala Gly Leu Thr Phe His Leu Leu Lys Asp Val Pro
                                 265
Gly Ile Val Ser Lys Asn Ile Asp Lys Ala Leu Ile Glu Ala Phe Gln
                             280
                                                 285
Pro Leu Asn Ile Ser Asp Tyr Asn Ser Ile Phe Trp Ile Ala His Pro
                        295
                                             300
Gly Gly Pro Ala Ile Leu Asp Gln Val Glu Glu Lys Leu Gly Leu Lys
                    310
                                         315
                                                             320
Pro Glu Lys Met Lys Ala Thr Arg Glu Val Leu Ser Glu Tyr Gly Asn
                325
                                     330
Met Ser Ser Ala Cys Val Leu Phe Ile Leu Asp Glu Met Arg Lys Lys
                                345
                                                     350
Ser Ala Gln Ala Gly Leu Lys Thr Thr Gly Glu Gly Leu Asp Trp Gly
                            360
Val Leu Phe Gly Phe Gly Pro Gly Leu Thr Ile Glu Thr Val Val Leu
    370
                        375
                                             380
His Ser Val Ala Ile
385
```

```
<210> 10
<211> 1242
<212> DNA
<213> Arabidopsis thaliana
```

<400> 10

```
ctcaactcta aattcgtccg agacgaagac gaacgcccta aagtcgctta caatgtgttt 60
agcgacgaaa tcccggtgat ctctctcgcc ggtatcgatg acgtcgatgg aaaaagagga 120
gagatctgcc gtcagatcgt cgaggcttgt gagaattggg gtatcttcca agtggttgat 180
cacggcgtcg atactaactt ggtggcggat atgactcgcc tcgctcgtga cttctttgct 240
ttacctccgg aagacaagct ccgtttcgac atgtccggtg gtaaaaaagg tggattcatc 300
gtctctagtc acctccaggt aaaagccaca ccacaatctt ctaggttaaa tacgtaatta 360
tgttttaatc ttgccgttaa agacataata attatactat aaatacaggg agaggctgtg 420
caagattgga gagagattgt aacgtatttc tcgtacccgg tgagaaacag agactactca 480
cggtggccaa ataagcctga aggatgggtg aaagtgacgg aggagtatag tgagaggctt 540
atgagtttgg cttgtaagct tcttgaggtt ttgtctgaag ctatgggtct tgagaaagag 600
tctcttacca atgcatgcgt cgatatggac caaaagattg ttgttaatta ttacccaaaa 660
tgccctcagc ctgatctcac cctcggactc aagcgtcaca ctgaccctgg aaccattacc 720
ttgctgctac aagaccaagt cggtggatta caagccacac gtgacaatgg caagacctgg 780
attacggttc agcctgttga aggagcgttt gtcgtcaatc tcggcgacca cggtcatgtt 840
agtactctat ccatttattg gcttttttgt ttctctgttt ttggttttga cttggtcaac 900
cttgatttgt cttgatgaag tttttgagca atgggaggtt caagaatgct gatcatcagg 960
ccgtggtgaa ctctaactcg agcagattat ccatagccac gttccagaac cccgcgccgg 1020
atgccacagt gtatccactg aaagtaagag aaggagagaa ggcaatattg gaggagccaa 1080
```

tcacgtttgc cgagatgtat aagagaaaga tgggaagaga tttggagctt gctcgcctca 1140 agaagctggc taaagaggag cgtgaccaca aagaagttgc caagcctgtc gaccaaatct 1200 tcgcttagaa tctctgtgtt cttgcttact tgttgttgcg tt 1242

<210> 11 <211> 342 <212> PRT

<213> Oryza sativa

<400> 11

Met Ala Ala Glu Ala Glu Gln Gln His Gln Leu Leu Ser Thr Ala Val 1 5 10 15

His Asp Thr Met Pro Gly Lys Tyr Val Arg Pro Glu Ser Gln Arg Pro
20 25 30

Arg Leu Asp Leu Val Val Ser Asp Ala Arg Ile Pro Val Val Asp Leu
35 40 45

Ala Ser Pro Asp Arg Ala Ala Val Val Ser Ala Val Gly Asp Ala Cys
50 60

Arg Thr His Gly Phe Phe Gln Val Val Asn His Gly Ile Asp Ala Ala 65 70 75 80

Leu Ile Ala Ser Val Met Glu Val Gly Arg Glu Phe Phe Arg Leu Pro 85 90 95

Ala Glu Glu Lys Ala Lys Leu Tyr Ser Asp Pro Ala Lys Lys Ile 100 105 110

Arg Leu Ser Thr Ser Phe Asn Val Arg Lys Glu Thr Val His Asn Trp
115 120 125

Arg Asp Tyr Leu Arg Leu His Cys Tyr Pro Leu His Gln Phe Val Pro 130 135 140

Asp Trp Pro Ser Asn Pro Pro Ser Phe Lys Glu Ile Ile Gly Thr Tyr 145 150 155 160

Cys Thr Glu Val Arg Glu Leu Gly Phe Arg Leu Tyr Glu Ala Ile Ser 165 170 175

Glu Ser Leu Gly Leu Glu Gly Gly Tyr Met Arg Glu Thr Leu Gly Glu 180 185 190

Gln Glu Gln His Met Ala Val Asn Tyr Tyr Pro Gln Cys Pro Glu Pro 195 200 205

Glu Leu Thr Tyr Gly Leu Pro Ala His Thr Asp Pro Asn Ala Leu Thr 210 215 220

Ile Leu Leu Met Asp Asp Gln Val Ala Gly Leu Gln Val Leu Asn Asp 225 230 235 240

Gly Lys Trp Ile Ala Val Asn Pro Gln Pro Gly Ala Leu Val Ile Asn

245 250 255

Ile Gly Asp Gln Leu Gln Ala Leu Ser Asn Gly Lys Tyr Arg Ser Val 260 265 Trp His Arg Ala Val Val Asn Ser Asp Arg Glu Arg Met Ser Val Ala 275 Ser Phe Leu Cys Pro Cys Asn Ser Val Glu Leu Gly Pro Ala Lys Lys 295 Leu Ile Thr Asp Asp Ser Pro Ala Val Tyr Arg Asn Tyr Thr Tyr Asp 305 310 315 Glu Tyr Tyr Lys Lys Phe Trp Ser Arq Asn Leu Asp Gln Glu His Cys 330 Leu Glu Leu Phe Arg Thr 340 <210> 12 <211> 815 <212> DNA <213> Juglans nigra <400> 12 gaggatgaga gacccaaggt tgcttacaat caattcagca ctgaaatccc catcatctcg 60 cttgccggga tagacgaagt ccatggccgg aggaccgaga tttgccagaa aatcgtcgag 120 gcctgtgagg actggggtat tttccaggtg gtcgatcatg gcgtcgatgc cagtctaatc 180 tecgacatga caegtettge cegtgactte ttegecatge etecegagga aaagettegt 240 ttcgacatgt ccggcggcaa gaagggcggt ttcattgtct ccagccatct gcaaggagaa 300 gcagtgcaag attggcgtga aattgtgaca tatttctcat acccaattag gaccagagac 360 tattcgaggt ggccggacaa gccagaaggg tggagaaagg tgacggagga gtacagtgac 420 aaattgatgg gactggcatg caaactgttg gaagtgctat cggaggcgat gggattagag 480 aaggaagcat tgaccaaggc ttgcgtggat atggaccaaa aggttgtggt taattactat 540 ccaaaatgtc cacagccaga cctcacattg gggctaaagc gccacacaga tcctggcacc 600 atcactctgt tgttgcagga ccaggtgggt gggcttcagg ccaccaggga tggcggcaag 660 acctggatca ctgttcagcc tgttgaagga gctttcgtcg tcaatcttgg agaccatggt 720 cattttctga gtaacgggag gttcaagaac gctgatcacc aagcagtggt gaactcaaac 780 tacagtcgat tgtccatcgc caccttccaa aaccc 815 <210> 13 <211> 815 <212> DNA <213> Juglans nigra <220> <221> CDS <222> (1) .. (813) <400> 13

gag gat gag aga ccc aag gtt gct tac aat caa ttc agc act gaa atc

Glu Asp Glu Arg Pro Lys Val Ala Tyr Asn Gln Phe Ser Thr Glu Ile

10

48

25334885.1 14

5

					gcc Ala			_	_	_						96
					atc Ile											144
_		-	_		ggc Gly	_	_	_	_				_	_		192
					ttc Phe 70											240
					ggc Gly											288
					gtg Val											336
					acc Thr	_	_		_			_	_	_		384
					gtg Val											432
					ttg Leu 150											480
_	_	_	_		aag Lys	_	_		-	_	_		_	_		528
					aaa Lys											576
					cct Pro											624
					gcc Ala											672
_	_		-	_	gga Gly 230	_		_	_				-			720
cat	ttt	ctg	agt	aac	ggg	agg	ttc	aag	aac	gct	gat	cac	caa	gca	gtg	768

His Phe Leu Ser Asn Gly Arg Phe Lys Asn Ala Asp His Gln Ala Val 245 250 255

gtg aac tca aac tac agt cga ttg tcc atc gcc acc ttc caa aac cc 815 Val Asn Ser Asn Tyr Ser Arg Leu Ser Ile Ala Thr Phe Gln Asn 260 265 270

<210> 14

<211> 271

<212> PRT

<213> Juglans nigra

<400> 14

Glu Asp Glu Arg Pro Lys Val Ala Tyr Asn Gln Phe Ser Thr Glu Ile 1 5 10 15

Pro Ile Ile Ser Leu Ala Gly Ile Asp Glu Val His Gly Arg Arg Thr 20 25 30

Glu Ile Cys Gln Lys Ile Val Glu Ala Cys Glu Asp Trp Gly Ile Phe 35 40 45

Gln Val Val Asp His Gly Val Asp Ala Ser Leu Ile Ser Asp Met Thr
50 55 60

Arg Leu Ala Arg Asp Phe Phe Ala Met Pro Pro Glu Glu Lys Leu Arg 65 70 75 80

Phe Asp Met Ser Gly Gly Lys Lys Gly Gly Phe Ile Val Ser Ser His 85 90 95

Leu Gln Gly Glu Ala Val Gln Asp Trp Arg Glu Ile Val Thr Tyr Phe
100 105 110

Ser Tyr Pro Ile Arg Thr Arg Asp Tyr Ser Arg Trp Pro Asp Lys Pro 115 120 125

Glu Gly Trp Arg Lys Val Thr Glu Glu Tyr Ser Asp Lys Leu Met Gly 130 135 140

Leu Ala Cys Lys Leu Leu Glu Val Leu Ser Glu Ala Met Gly Leu Glu 145 150 155 160

Lys Glu Ala Leu Thr Lys Ala Cys Val Asp Met Asp Gln Lys Val Val
165 170 175

Val Asn Tyr Tyr Pro Lys Cys Pro Gln Pro Asp Leu Thr Leu Gly Leu 180 185 190

Lys Arg His Thr Asp Pro Gly Thr Ile Thr Leu Leu Gln Asp Gln
195 200 205

Val Gly Gly Leu Gln Ala Thr Arg Asp Gly Gly Lys Thr Trp Ile Thr 210 215 220

Val Gln Pro Val Glu Gly Ala Phe Val Val Asn Leu Gly Asp His Gly

225 230 235 240

His Phe Leu Ser Asn Gly Arg Phe Lys Asn Ala Asp His Gln Ala Val 245 250 255

Val Asn Ser Asn Tyr Ser Arg Leu Ser Ile Ala Thr Phe Gln Asn 260 265 270